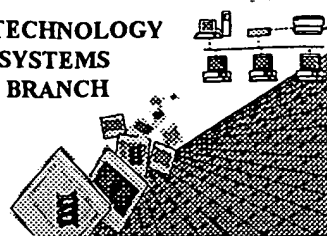


0360-0362
0278/036
BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/964,059
Source: 01/E
Date Processed by STIC: 2/5/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER** **VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/964,059

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/964,059

DATE: 02/05/2002
TIME: 16:24:59

Input Set : N:\EBONY'S\ES.txt
Output Set: N:\CRF3\02052002\I964059.raw

**Does Not Comply
Corrected Diskette Needed**

1 <110> APPLICANT: Frudakis, Tony
3 <120> TITLE OF INVENTION: Efficient Methods and Apparatus for High-Throughput
Processing
4 of Gene Sequence Data
6 <130> FILE REFERENCE: 0201-0001
8 <140> CURRENT APPLICATION NUMBER: US 09/964,059
10 <141> CURRENT FILING DATE: 2001-09-26
12 <150> PRIOR APPLICATION NUMBER: US 60/274,686
13 <151> PRIOR FILING DATE: 2000-03-08
15 <160> NUMBER OF SEQ ID NOS: 239

ppr 1-6

ERRORED SEQUENCES

181 <210> SEQ ID NO: 17
182 <211> LENGTH: 3260 3360 (p. 2)
183 <212> TYPE: DNA
184 <213> ORGANISM: Homo Sapiens
186 <400> SEQUENCE: 17

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189	aacagattaa	actgactttt	acagaataat	tattctttta	ccttgtttac	atggaaagga	180
190	atcctccatt	ttaggatgca	cataaaatgc	cagcctatgt	tgatgacatt	gccttaacac	240
191	ttttttttta	agtaatttta	cagggtagtt	aacctgtaaa	agaaacagtg	gataaacttg	300
192	aaaatgctaa	tagcaaaaaa	cacttcagcc	atggcacata	caaccagaag	ccaatgatat	360
193	ccttcaacta	tagaaattag	cggtgttttc	tgtttattcc	tgaagcagga	ttccatattc	420
194	aagccagaaa	ttgtcattca	acagaaaaaa	tcaggtcaaa	acaatcaatc	acataatgta	480
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206	aggtaagtag	gcttgaaaac	ccttggaaac	tgagcagttc	tattttgaac	tagcatgttt	1200
207	taatcaaagg	tatggaatta	atcaaataatc	aattaagaat	tactggaatg	cacactcatg	1260
208	ccaaatgaca	actaacatgt	tatttcctac	tatgatgact	ctttgatttg	agtcagatgg	1320
209	cataaaaaaa	tattgctagc	tatacaataa	attttactct	tctgcttctg	ctctctaaag	1380
210	aaaaatctta	ttttttcaca	taagaagctc	atggaatcga	atgttaatta	aagaaaagat	1440
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RAW SEQUENCE LISTING

DATE: 02/05/2002

PATENT APPLICATION: US/09/964,059

TIME: 16:24:59

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Output Set: N:\CRF3\02052002\I964059.raw

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213 tcatgagcct cggccacctt ctccaatgga tattgagaac ctatcacagg tttcaaccag 1620
214 ccaatttcca ttccagcttg aagggtctgt gcatattgct gaaattcctc ctaagaaaag 1680
215 gaaaaacaaa tttctttttg tagtgaaccg tatgatttaa ttttcagaag cattaaaaac 1740
E--> 216 acttcagaat ctaagtgtta taccatgaag agtctcttac aaatgtgtga cttttgtcaa 1700 1800
E--> 217 cttgtccaga actatagaaa aagtagttat ctacagggtta accataaatc ccatctgcct 1760
E--> 218 gagacagtgt tagtgtacaa aatacctgtt gtcttgaaat tattactagt atcacatttc 1820
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E--> 220 gtgactaatc cttaccaact cccactagtc atataactaa gtttaacatc tattcaaact 1940
E--> 221 ttcagcttgc ctgagtaggc aaactgtacc aatgtttaag ttaccaaact cagaagtact 2000
E--> 222 tcttttcceta ccttggttga ggaaaagaga gtaactccaa ttatactcga ctctttgccc 2060
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341 <210> SEQ ID NO: 20

342 <211> LENGTH: 384

343 <212> TYPE: DNA

344 <213> ORGANISM: Homo Sapiens

346 <400> SEQUENCE: 20

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348 agcttaaaga tagtccaaac gcaaagctgt ctttaaaaaa tgcatactct attactggca 120

349 acaaagtttt ataattctata cattttatga accactaatc ctttaatttat tcaagatcac 180

350 aacaggggac tcatattata gagtcaagta aatatcatta ccaacatttt atttaacagt 240

351 ttgtcctcct taattacatg gagaatgata tagtgactcc ttcatgcctt tttttctcct 300

352 taacaagcca tatgcaggaa agtttccatg ctgcgcaaac ataaaagaaa gttatatttc 360

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574 <212> TYPE: DNA

575 <213> ORGANISM: Homo Sapiens

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578 attctaactg cagagctcta acttttccct ctaagctcct gagaggcaga ttggcagcta 60

1700 1800

numbering
off

see item 9 on Enr Summary Sheet

RAW SEQUENCE LISTING

DATE: 02/05/2002

PATENT APPLICATION: US/09/964,059

TIME: 16:24:59

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E--> 580 aagttctgag tctctctccc ccattccccc acattagcat tttcagccat gggttgtggt 240 180
E--> 581 gttaaggaca gggctgtata cgtgcactcc atggatgtca tcaaagtga gcaggcaagc 360
E--> 582 agcagaagg agatagaagg actaagaatt cacagtgtgg ctttaccgtg ctgtctgggg 480
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585 aggcaaaaaac aaggccagtt tatcttagtc tacacccaat acaggtggaa aatctaacat 480
E--> 586 atttttgaag ggggtgctctg ttgagtttat taaccaagaa atgctaaact aatgacaaaa 960
E--> 587 catcaccttc agaagaccaa aatcaaaagt tttactacat aaagaaaaaa agcaccttg 1080
E--> 588 actctattta taaatctgac ttttaaaaaat gaccaaagga actataatgt gaaaccata 1140
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E--> 590 accagaacac tctctccagc tttcacacag gcaactgcaa ggaaagcata agttacatca 1260
E--> 591 ccttattttt tgaagctaat taatctcggt tgttttcac atcttaagga atttctacce 1320
E--> 592 ctagtctggc taacacttac acaaacagca aatgcaacct gacatacagc cccaaatatt 1380
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816 <210> SEQ ID NO: 63

817 <211> LENGTH: 1300

818 <212> TYPE: DNA

819 <213> ORGANISM: Homo Sapiens

821 <400> SEQUENCE: 63

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825 ttataagcat atatattagg ttattaggac tcataaattt atgttattta cttccagttt 240
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829 cactaatggt cagaagagca tatgatattg ctggatccac caaagatgtc aaagtccttc 480
830 ttaatggaaa taaactgcca tgagtatttt cctggatgtt aaggataata agggattttg 540
831 taatcattgt caagtgcaaa attgaatttt tccccctccc atatgttttt gtttgtttgt 600
832 ttgtttgttt gtttgagaca gagtctcaca ctgttgcccg ggctggagtg cagtggcacg 660
833 atctcggtc accgcaacct ccacctccca ggttcacgca attctcctgc ctacgctcc 720
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835 agagacaggt ttcactatgt tggccaggct ggtctogaac accagacctc atgatccacc 840
836 cgtcttggtc tcccaaagtg ctgggattac aggcattgag cactgcacct ggcccaacca 900
837 tatgtatttt cttaccactt ctacatatg ttcttgaaaa gagaatggta tgccacattt 960
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/964,059

DATE: 02/05/2002

TIME: 16:24:59

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842 gcccagctaa tttttttttt tctttttaat agaggtgggg atctcactat gttgcccagg 1260
843 ctggtcttga actcctgggc tcaagtgate caccacctc          1300
1581 <210> SEQ ID NO: 146
1582 <211> LENGTH: 41
1583 <212> TYPE: DNA
1584 <213> ORGANISM: Homo Sapiens
1586 <400> SEQUENCE: 146
E--> 1587 aggggtaga ttttaaaaat (n)catgttaat gttatttact (n) 41 -> item 9
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1590 <211> LENGTH: 41
1591 <212> TYPE: DNA
1592 <213> ORGANISM: Homo Sapiens
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1599 <212> TYPE: DNA
1600 <213> ORGANISM: Homo Sapiens
1602 <400> SEQUENCE: 148
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1606 <211> LENGTH: 41
1607 <212> TYPE: DNA
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1615 <212> TYPE: DNA
1616 <213> ORGANISM: Homo Sapiens
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1622 <211> LENGTH: 41
1623 <212> TYPE: DNA
1624 <213> ORGANISM: Homo Sapiens
1626 <400> SEQUENCE: 151
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1630 <211> LENGTH: 41
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1691 <212> TYPE: DNA
1692 <213> ORGANISM: Homo Sapiens

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/964,059

DATE: 02/05/2002
TIME: 16:25:00

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Output Set: N:\CRF3\02052002\I964059.raw

1694 <400> SEQUENCE: 158
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1697 <210> SEQ ID NO: 159
1698 <211> LENGTH: 11
1699 <212> TYPE: DNA
1700 <213> ORGANISM: Homo Sapiens
1702 <400> SEQUENCE: 159
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1705 <210> SEQ ID NO: 160
1706 <211> LENGTH: 11
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1710 <400> SEQUENCE: 160
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1713 <210> SEQ ID NO: 161
1714 <211> LENGTH: 11
1715 <212> TYPE: DNA
1716 <213> ORGANISM: Homo Sapiens
1718 <400> SEQUENCE: 161
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1721 <210> SEQ ID NO: 162
1722 <211> LENGTH: 11
1723 <212> TYPE: DNA
1724 <213> ORGANISM: Homo Sapiens
1726 <400> SEQUENCE: 162
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1729 <210> SEQ ID NO: 163
1730 <211> LENGTH: 11
1731 <212> TYPE: DNA
1732 <213> ORGANISM: Homo Sapiens
1734 <400> SEQUENCE: 163
E--> 1735 cttctgagtt a 11 *7 item 9*
1737 <210> SEQ ID NO: 164
1738 <211> LENGTH: 11
1739 <212> TYPE: DNA
1740 <213> ORGANISM: Homo Sapiens
1742 <400> SEQUENCE: 164
E--> 1743 cttctgagtt a 11 *7 item 9*
1745 <210> SEQ ID NO: 165
1746 <211> LENGTH: 11
1747 <212> TYPE: DNA
1748 <213> ORGANISM: Homo Sapiens
1750 <400> SEQUENCE: 165
E--> 1751 cttctgagtt a 11 *7 item 9*
1753 <210> SEQ ID NO: 166
1754 <211> LENGTH: 11
1755 <212> TYPE: DNA
1756 <213> ORGANISM: Homo Sapiens
1758 <400> SEQUENCE: 166

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RAW SEQUENCE LISTING

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E--> 1759 qntctgagtt a 11 → *item 9*
 1761 <210> SEQ ID NO: 167
 1762 <211> LENGTH: 11
 1763 <212> TYPE: DNA
 1764 <213> ORGANISM: Homo Sapiens
 1766 <400> SEQUENCE: 167

E--> 1767 qntctgagtt a 11 → *item 9*
 1769 <210> SEQ ID NO: 168
 1770 <211> LENGTH: 11
 1771 <212> TYPE: DNA
 1772 <213> ORGANISM: Homo Sapiens
 1774 <400> SEQUENCE: 168

E--> 1775 qntttgagtt a 11 → *item 9* → The types of errors shown exist throughout
 2332 <210> SEQ ID NO: 238 the Sequence Listing. Please check subsequent
 2333 <211> LENGTH: (260) 200 sequences for similar errors.
 2334 <212> TYPE: DNA
 2335 <213> ORGANISM: Homo Sapiens
 2337 <400> SEQUENCE: 238
 2338 ctcagggtccc acagcaacaa tatcattcaa actgcaatta aaacatacac acataatata 60

E--> 2339 taaggtgaag gtattgaaca ttacaggatt attaactggc attcctcact gtctattcct (180) 120
 E--> 2340 aaaatcaaga tgtgggatgg agccttcgtg ctagctataa tggaacacaa ttaatatgaa (240) 180
 E--> 2341 attagtctctg ccgatacaat (260) 200

see next page

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end
of
file

VERIFICATION SUMMARY

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L:216 M:254 E: No. of Bases conflict, LENGTH:Input:1700 Counted:1800 SEQ:17
M:254 Repeated in SeqNo=17
L:242 M:252 E: No. of Seq. differs, <211>LENGTH:Input:3260 Found:3360 SEQ:17
L:353 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:20
L:580 M:254 E: No. of Bases conflict, LENGTH:Input:240 Counted:180 SEQ:36
M:254 Repeated in SeqNo=36
L:603 M:252 E: No. of Seq. differs, <211>LENGTH:Input:2037 Found:1557 SEQ:36
L:822 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:63
L:1587 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:146
L:1595 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:147
L:1603 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:148
L:1611 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:149
L:1619 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:150
L:1627 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:151
L:1635 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:152
L:1695 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:158
L:1703 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:159
L:1711 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:160
L:1719 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:161
L:1727 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:162
L:1735 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:163
L:1743 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:164
L:1751 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:165
L:1759 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:166
L:1767 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:167
L:1775 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:168
L:1783 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:169
L:1791 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:170
L:1799 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:171
L:1807 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:172
L:1815 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:173
L:1823 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:174
L:1831 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:175
L:1847 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:177
L:1855 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:178
L:1863 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:179
L:1871 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:180
L:1879 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:181
L:1887 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:182
L:1895 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:183
L:1903 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:184
L:1911 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:185
L:1919 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:186
L:1927 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:187
L:1935 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:188
L:1943 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:189
L:1951 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:190
L:1959 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:191

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L:1967 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:192
 L:1975 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:193
 L:1983 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:194
 L:1991 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:195
 L:2023 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:199
 L:2031 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:200
 L:2063 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:204
 L:2079 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:206
 L:2339 M:254 E: No. of Bases conflict, LENGTH:Input:180 Counted:120 SEQ:238
 M:254 Repeated in SeqNo=238
 L:2341 M:252 E: No. of Seq. differs, <211>LENGTH:Input:260 Found:200 SEQ:238
 L:2352 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:5
 L:2353 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:239
 L:2353 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:5